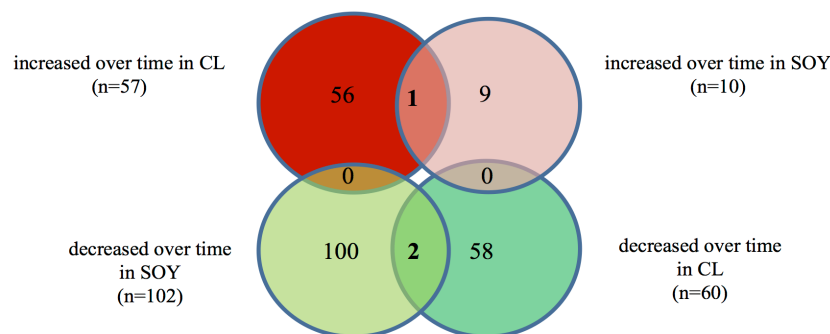


Supplementary Figure 3

A Gene expression change across adolescence:



Venn diagram based on sets of genes filtered by Paired t-test: unadjusted $P < 0.05$; Fold-change > 1.5
 $n = 4$ monkeys per diet group

B Top 10 differentially expressed genes:

	at 7-12 months post-menarche (n=157 genes)	FC	P-value	at 19-24 months post-menarche (n=190 genes)	FC	P-value
upregulated in SOY (vs. CL)	<i>NBEAL2-like</i>	6.74	0.041	<i>LEP</i>	2.62	0.041
	<i>TFF3-homolog</i>	3.11	0.028	<i>CA6-like</i>	2.62	0.042
	<i>ALDH9A1-like</i>	2.79	0.049	<i>MIR675</i>	2.58	0.003
	<i>CPA3</i>	2.73	0.015	<i>PPIA-like</i>	2.38	0.001
	<i>DPT</i>	2.40	0.034	<i>STX3-like</i>	2.27	0.017
downregulated in SOY (vs. CL)	<i>RPLP2-like</i>	1.99	0.040	<i>CXCL9</i>	4.38	0.006
	<i>ANKRD62-like</i>	1.99	0.027	<i>CXCL10</i>	2.88	0.034
	<i>CAPN3</i>	1.94	0.021	<i>RTD1B</i>	2.41	0.006
	<i>FAM3B-like</i>	1.83	0.006	<i>DPPA2</i>	2.33	0.019
	<i>ZNF850</i>	1.83	0.017	<i>IGLV7-46</i>	2.05	0.005

$n = 4$ monkeys per diet group

Filtered by $FC > 1.5$; unadjusted $P < 0.05$ (by empirical Bayes)

C Gene enrichment analysis:

	Top-10 significantly enriched KEGG gene sets (FDR<0.05)					
	CL	Size	FDR	SOY	Size	FDR
Enriched among genes that were upregulated over time	Olfactory transduction	128	0.00	Ribosome	60	0.01
	Neuroactive ligand receptor interaction	207	0.00	Olfactory transduction	128	0.01
	Autoimmune thyroid disease	26	0.00			
	Cytokine-cytokine receptor interaction	212	0.00			
	Intestinal immune network for IgA production	34	0.00			
Enriched among genes that were down-regulated over time	Spliceosome	93	0.00	ECM receptor interaction	70	0.00
	Valine, leucine, isoleucine degradation	28	0.00	Focal adhesion	159	0.00
	Huntington disease	126	0.00	TGF-beta signaling pathway	68	0.00
	Insulin signaling pathway	107	0.00	Adherens junction	59	0.01
	Arrhythmogenic right ventricular cardiomyopathy	59	0.00			

Supplementary Figure 3. Gene expression profile in the post-menarchal macaque breast by microarray. (A) Venn diagram showing number of genes that changed with time (i.e. between 7-12 months to 18-24 months after menarche) in the control (CL) and soy group (SOY), based on unadjusted P -values from a paired t-test in each diet group. (B) The list of top-10 genes that showed significant difference by dietary treatment using empirical Bayes statistics. (C) The top-10 significantly enriched KEGG pathways in CL and SOY groups across time. FC = fold-change; FDR=false discovery rate.